

SEQ ID NO: 1

CGGGGAGGAATATGCTGTGGAGCTCCTCTGCCATATAAACAAAAAGAGGAAATCTTTCAA 60
ACATGGCTGAAGCAAAGACCCACTGGCTTGGAGCAGCCCTGTCTCTTATCCCTTTAATTT 120
5 TCCTCATCTCTGGGGCTGAAGCAGCTTCATTTTCAGAGAAACCAGCTGCTTCAGAAAGAAC 180
CAGACCTCAGGTTGGAAAATGTCCAAAAGTTTCCCAGTCCTGAAATGATCAGGGCTTTGG 240
AGTACATAGAAAACCCCTTTTAAACGCACAAATGAAATAGTGGAGGAACAATATACTCCTC 300
AAAGCCTTGCTACATTGGAATCTGTCTTCCAAGAGCTGGGGAAACTGACAGGACCAAACA 360
ACCAGAAACGTGAGAGGATGGATGAGGAGCAAAAACCTTTATACGGATGATGAAGATGATA 420
10 TCTACAAGGCTAATAACATTGCCTATGAAGATGTGGTTCGGGGGAGAAGACTGGAACCCAG 480
TAGAGGAGAAAAATAGAGAGTCAAACCCAGGAAGAGGTGAGAGACAGCAAAGAGAATATAG 540
GAAAAAATGAACAAATCAACGATGAGATGAAACGCTCAGGGCAGCTTGGCATCCAGGAAG 600
AAGATCTTCGGAAAGAGAGTAAAGACCAACTCTCAGATGATGTCTCCAAAGTAATTGCCT 660
ATTTGAAAAGGTTAGTAAATGCTGCAGGAAGTGGGAGGTTACAGAATGGGCAAAATGGGG 720
15 AAAGGGCCACCAGGCTTTTTGAGAAACCTCTTGATTCTCAGTCTATTTATCAGCTGATTG 780
AAATCTCAAGGAATTTACAGATACCCCCAGAAGACTTAATTGAGATGCTCAAACTGGGG 840
AGAAGCCGAATGGATCAGTGGAACCGGAGCGGGAGCTTGACCTTCCTGTTGACCTAGATG 900
ACATCTCAGAGGCTGACTTAGACCATCCAGACCTGTTCCAAAATAGGATGCTCTCCAAGA 960
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20 TTGAGGATATTTTAAATCTTTTAGGGATGGAGAGTGCAGCAAATCAGAAAACGTCGTATT 1080
TTCCCAATCCATATAACCAGGAGAAAGTTCTGCCAAGGCTCCCTTATGGTGCTGGAAGAT 1140
CTAGATCGAACCAGCTTCCCAAAGCTGCCTGGATTCCACATGTTGAAAACAGACAGATGG 1200
CATATGAAAACCTGAACGACAAGGATCAAGAATTAGGTGAGTACTTGGCCAGGATGCTAG 1260
TTAAATACCCTGAGATCATTAATTCAAACCAAGTGAAGCGAGTTCCTGGTCAAGGCTCAT 1320
25 CTGAAGATGACCTGCAGGAAGAGGAACAAATTGAGCAGGCCATCAAAGAGCATTTGAATC 1380
AAGGCAGCTCTCAGGAGACTGACAAGCTGGCCCCGGTGAGCAAAAGGTTCCCTGTGGGGC 1440
CCCCGAAGAATGATGATACCCCCAAATAGGCAGTACTGGGATGAAGATCTGTTAATGAAAG 1500
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CAATGGAAAAATATGTAAGCTGCTTTCATTAATTACCCTACTTTCATTCTCCACCCCCAA 1620
30 GCAAAATCCCAACATTTCTCTTCAGTGTGTTGACTTCTATCCTGTAACTGTAATATCT 1680
TTAAATGATGTACAGGCAGATGAAACCAGGTCCTGGGGAGTCTGCTTCATTTCTCTGA 1740
GCTGTTATCTTGTGTATGGATATGTGTAAATGTTATGACTCCTTGATAAAAAATTTATTA 1800
TGTCCATTATTCAAGAAAGATATCTATGACTGTGTTTAATAGTATATCTAATGGCTGTGG 1860
CATTGTTGATGCTCACATATGATAAAAAAGTGTCTCTATAATTCTATTGAAAGTTTTTAAT 1920
35 ATTTATTGAATTATTTTGTACTGTCTGTAGCGTTTTGTGGAGTACTGGACCAAAAAAAT 1980
AAAGCATTATAAATATA 1997

SEQ ID NO: 2

	Met	Ala	Glu	Ala	Lys	Thr	His	Trp	Leu	Gly	10
5	Ala	Ala	Leu	Ser	Leu	Ile	Pro	Leu	Ile	Phe	20
	Leu	Ile	Ser	Gly	Ala	Glu	Ala	Ala	Ser	Phe	30
	Gln	Arg	Asn	Gln	Leu	Leu	Gln	Lys	Glu	Pro	40
	Asp	Leu	Arg	Leu	Glu	Asn	Val	Gln	Lys	Phe	50
	Pro	Ser	Pro	Glu	Met	Ile	Arg	Ala	Leu	Glu	60
10	Tyr	Ile	Glu	Asn	Pro	Phe	Lys	Arg	Thr	Asn	70
	Glu	Ile	Val	Glu	Glu	Gln	Tyr	Thr	Pro	Gln	80
	Ser	Leu	Ala	Thr	Leu	Glu	Ser	Val	Phe	Gln	90
	Glu	Leu	Gly	Lys	Leu	Thr	Gly	Pro	Asn	Asn	100
	Gln	Lys	Arg	Glu	Arg	Met	Asp	Glu	Glu	Gln	110
15	Lys	Leu	Tyr	Thr	Asp	Asp	Glu	Asp	Asp	Ile	120
	Tyr	Lys	Ala	Asn	Asn	Ile	Ala	Tyr	Glu	Asp	130
	Val	Val	Gly	Gly	Glu	Asp	Trp	Asn	Pro	Val	140
	Glu	Glu	Lys	Ile	Glu	Ser	Gln	Thr	Gln	Glu	150
	Glu	Val	Arg	Asp	Ser	Lys	Glu	Asn	Ile	Gly	160
20	Lys	Asn	Glu	Gln	Ile	Asn	Asp	Glu	Met	Lys	170
	Arg	Ser	Gly	Gln	Leu	Gly	Ile	Gln	Glu	Glu	180
	Asp	Leu	Arg	Lys	Glu	Ser	Lys	Asp	Gln	Leu	190
	Ser	Asp	Asp	Val	Ser	Lys	Val	Ile	Ala	Tyr	200
	Leu	Lys	Arg	Leu	Val	Asn	Ala	Ala	Gly	Ser	210
25	Gly	Arg	Leu	Gln	Asn	Gly	Gln	Asn	Gly	Glu	220
	Arg	Ala	Thr	Arg	Leu	Phe	Glu	Lys	Pro	Leu	230
	Asp	Ser	Gln	Ser	Ile	Tyr	Gln	Leu	Ile	Glu	240
	Ile	Ser	Arg	Asn	Leu	Gln	Ile	Pro	Pro	Glu	250
	Asp	Leu	Ile	Glu	Met	Leu	Lys	Thr	Gly	Glu	260
30	Lys	Pro	Asn	Gly	Ser	Val	Glu	Pro	Glu	Arg	270
	Glu	Leu	Asp	Leu	Pro	Val	Asp	Leu	Asp	Asp	280
	Ile	Ser	Glu	Ala	Asp	Leu	Asp	His	Pro	Asp	290
	Leu	Phe	Gln	Asn	Arg	Met	Leu	Ser	Lys	Ser	300
	Gly	Tyr	Pro	Lys	Thr	Pro	Gly	Arg	Ala	Gly	310
35	Thr	Glu	Ala	Leu	Pro	Asp	Gly	Leu	Ser	Val	320
	Glu	Asp	Ile	Leu	Asn	Leu	Leu	Gly	Met	Glu	330
	Ser	Ala	Ala	Asn	Gln	Lys	Thr	Ser	Tyr	Phe	340
	Pro	Asn	Pro	Tyr	Asn	Gln	Glu	Lys	Val	Leu	350

	Pro	Arg	Leu	Pro	Tyr	Gly	Ala	Gly	Arg	Ser	360
	Arg	Ser	Asn	Gln	Leu	Pro	Lys	Ala	Ala	Trp	370
	Ile	Pro	His	Val	Glu	Asn	Arg	Gln	Met	Ala	380
	Tyr	Glu	Asn	Leu	Asn	Asp	Lys	Asp	Gln	Glu	390
5	Leu	Gly	Glu	Tyr	Leu	Ala	Arg	Met	Leu	Val	400
	Lys	Tyr	Pro	Glu	Ile	Ile	Asn	Ser	Asn	Gln	410
	Val	Lys	Arg	Val	Pro	Gly	Gln	Gly	Ser	Ser	420
	Glu	Asp	Asp	Leu	Gln	Glu	Glu	Glu	Gln	Ile	430
	Glu	Gln	Ala	Ile	Lys	Glu	His	Leu	Asn	Gln	440
10	Gly	Ser	Ser	Gln	Glu	Thr	Asp	Lys	Leu	Ala	450
	Pro	Val	Ser	Lys	Arg	Phe	Pro	Val	Gly	Pro	460
	Pro	Lys	Asn	Asp	Asp	Thr	Pro	Asn	Arg	Gln	470
	Tyr	Trp	Asp	Glu	Asp	Leu	Leu	Met	Lys	Val	480
	Leu	Glu	Tyr	Leu	Asn	Gln	Glu	Lys	Ala	Glu	490
15	Lys	Gly	Arg	Glu	His	Ile	Ala	Lys	Arg	Ala	500
	Met	Glu	Asn	Met							504

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CGGGGAGGAATATGCTGTGGAGCTCCTCTGCCATATAAAACAAAAGAGGAAATCTTTCAA 60
ACATGGCTGAAGCAAAGACCCACTGGCTTGGAGCAGCCCTGTCTCTTATCCCTTTAATTT 120
TCCTCATCTCTGGGGCTGAAGCAACAGCTTCATTTCCAGTCTGTAAGCAAAATGAAATAGT 180
CAGACCTCAGGTTGGAATGTCCAAAGCTTCCAGGATAACCCCTTTAAACGCACAAATGAAATAGT 240
AGTACATAGAAAACCTCCGACAAACAGCTCATAAGAAAGAAAGCTTAAGCAAAATGAAATAGT 300
CCCTCCTATGTATGAAGAGAAATTCAGGCTTGTACATTGGAATCTGTCTTCCAGAGCTGGG 360
GGAGGAACAATATACTCCTCAAAGCCTTGCTACATTGGAATCTGTCTTCCAGAGCTGGG 420
GAAACTGACAGGACCAACCAAGGCTTGTACATTGGAATCTGTCTTCCAGAGCTGGG 480
TACGGATGATGAAGATGATATCTACAAGGCTAATAACATTGCCTATGAAGATGTGGTGG 540
GGGAGAAGACTGGAACCCAGTAGAGGAGAAATAGAGAGTCAAAACCCAGGAAGAGGTGAG 600
AGACAGCAAAAGAGAAATATAGGAAAAATGAAACAAATAGAGAGTAAAGACCAACTCTCAGATGA 660
GCAGCTTGGCATCCAGGAAGAAGATCTTCGGAAGGCTTGTAGTAAAGACCAACTCTCAGATGA 720
TGTCTCAAAGTAATTGCCTATTGAAAAGGCTTGTAGTAAAGACCAACTCTCAGATGA 780
ACAGAAATGGGCAAAATGGGAAAGGCTTGTAGTAAAGACCAACTCTCAGATGA 840
GTCTATTTATCAGCTGATTGAAAAGGCTTGTAGTAAAGACCAACTCTCAGATGA 900
TGAGATGCTCAAAACTGGGAGAGGCTTGTAGTAAAGACCAACTCTCAGATGA 960
CCTTCTGTGCTCCTCAAGAGTGGCTACCTTAAACCTTGTAGGAGTGGAGTGCAGC 1020
AAATAGGATGCTCCTCAAGAGTGGCTACCTTAAACCTTGTAGGAGTGGAGTGCAGC 1080
AAATCAGAAAACGCTCAGTGTGAGGATATTTTAAACCTTGTAGGAGTGGAGTGCAGC 1140
CCCTTATGGTGTGGAAGATCTAGATCGAACCAGCTTCCCAAAGCTGCCTGGATTCCACA 1200
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GTACTTGGCCAGGATGCTAGTTAAATACCTGAGATCATTAAATCAAGGATCAAGAAATAGGTGA 1320
AGTTCTCTGGTCAAGGCTCATCTGAAGATGACCTGAGGAGGAAACAAATAGGTGA 1380
CATCAAAGAGCATTTGAATCAAGGCAGCTCTCAGGAGGAAACAAATAGGTGA 1440
CAAAAGGTTCCCTGTGGGCCCCGGAAGATGATGTAAGCTGCTTCAATTAATTACCTATC 1500
TGAAGATCTGTTAATGAAAGTGCTGGAATACCTCAATCAAGAAAGGAGGAAAG 1560
GGAGCATATTGCTAAGAGCAATGGAAATATGTAAGCTGCTTCAATTAATTACCTATC 1620
TTTCATTCTCCCAACCAAGCAATGATGTAAGCTGCTTCAATTAATTACCTATC 1680
CTGTAAACACTGTAATATCTTTAAATGATGTACAGGAGGAAACAAATAGGTGA 1740
GTCTGCTTCAATTTCTGAGCTGTTATCTGTGATGATGTAAGCTGCTTCAATTAATTACCTATC 1800
CCTTGATAAAAAATTTATATGTCATTATTCAAGAAAGATATGTAAGCTGCTTCAATTAATTACCTATC 1860
AGTATATCTAATGGCTGTGGCATTGTTGATGCTCACATATGATAAAAAAGTGTCTTAAAT 1920
TTCTATTGAAAGTTTTTAATATTTATGATGCTCACATATGATAAAAAAGTGTCTTAAAT 1980
GAGTACTGGACCAAAAAATAAGCATTATAAAATATA 2040
2077

SEQ ID NO: 4

	Met	Ala	Glu	Ala	Lys	Thr	His	Trp	Leu	Gly	10
	Ala	Ala	Leu	Ser	Leu	Ile	Pro	Leu	Ile	Phe	20
5	Leu	Ile	Ser	Gly	Ala	Glu	Ala	Ala	Ser	Phe	30
	Gln	Arg	Asn	Gln	Leu	Leu	Gln	Lys	Glu	Pro	40
	Asp	Leu	Arg	Leu	Glu	Asn	Val	Gln	Lys	Phe	50
	Pro	Ser	Pro	Glu	Met	Ile	Arg	Ala	Leu	Glu	60
	Tyr	Ile	Glu	Asn	Leu	Arg	Gln	Gln	Ala	His	70
10	Lys	Lys	Glu	Ser	Leu	Ser	Thr	Cys	Asn	Ser	80
	Leu	Leu	Cys	Met	Lys	Arg	Ile	Pro	Gly	Ile	90
	Thr	Pro	Leu	Asn	Ala	Gln	Met	Lys			98

SEQ ID NO: 5

CGGGGAGGAATATGCTGTGGAGCTCCTCTGCCATATAAACAAAAAGAGGAAATCTTTCAA 60
ACATGGCTGAAGCAAAGACCCACTGGCTTGGAGCAGCCCTGTCTCTTATCCCTTTAATTT 120
5 TCCTCATCTCTGGGGCTGAAGCAGCTTCATTTTCAGAGAAACCAGCTGCTTCAGAAAGAAC 180
CAGACCTCAGGTTGGAAAATGTCCAAAAGTTTCCCAGTCCTGAAATGATCAGGGCTTTGG 240
AGTACATAGAAAACCTCCGACAACAAGCTCATAAGGAAGAAAGCAGCCCAGATTATAATC 300
CCTACCAAGGTGTCTCTGTCCCCCTTCAGCAAAAAGAAAATGGCGATGAAAGCCACTTGC 360
CCGAGAGGGATTCACTGAGTGAAGAAGACTGGATGAGAATAATACTCGAAGCTTTGAGAC 420
10 AGGCTGAAAATGAGCCTCAGTCTGCACCAAAAAGAAAATAAGCCCTATGCCTTGAATTCAG 480
AAAAGAACTTTCCAATGGACATGAGTGATGATTATGAGACACAGCAGTGGCCAGAAAGAA 540
AGCTTAAGCACATGCAATTCCCTCCTATGTATGAAGAGAATTCCAGGGATAACCCCTTTA 600
AACGCACAAATGAAATAGTGGAGGAACAATATACTCCTCAAAGCCTTGCTACATTGGAAT 660
CTGTCTTCCAAGAGCTGGGGAAACTGACAGGACCAACAACCAGAAACGTGAGAGGATGG 720
15 ATGAGGAGCAAAAACCTTTATACGGATGATGAAGATGATATCTACAAGGCTAATAACATTG 780
CCTATGAAGATGTGGTCGGGGGAGAAGACTGGAACCCAGTAGAGGAGAAAATAGAGAGTC 840
AAACCCAGGAAGAGGTGAGAGACAGCAAAGAGAATATAGGAAAAAATGAACAAATCAACG 900
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AAGACCAACTCTCAGATGATGTCTCCAAAGTAATTGCCTATTTGAAAAGGTTAGTAAATG 1020
20 CTGCAGGAAGTGGGAGGTTACAGAAATGGGCAAAATGGGGAAAGGGCCACCAGGCTTTTTG 1080
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AACCGGAGCGGGAGCTTGACCTTCCTGTTGACCTAGATGACATCTCAGAGGCTGACTTAG 1260
ACCATCCAGACCTGTTCCAAAATAGGATGCTCTCCAAGAGTGGCTACCCTAAAACACCTG 1320
25 GTCGTGCTGGGACTGAGGCCCTACCAGACGGGCTCAGTGTTGAGGATATTTTAAATCTTT 1380
TAGGGATGGAGAGTGCAGCAAATCAGAAAACGTCGTATTTTCCCAAGCAAATCCCAACAT 1440
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TATGGATATGTGTAAATGTTATGACTCCTTGATAAAAAATTTATTATGTCCATTATTCAA 1620
30 GAAAGATATCTATGACTGTGTTTAATAGTATATCTAATGGCTGTGGCATTGTTGATGCTC 1680
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TTTGTACTGTCTGTAGCGTTTTTGTGGAGTACTGGACCAAAAAAATAAAGCATTATAAAT 1800
ATA 1803

SEQ ID NO: 6

	Met	Ala	Glu	Ala	Lys	Thr	His	Trp	Leu	Gly	10
5	Ala	Ala	Leu	Ser	Leu	Ile	Pro	Leu	Ile	Phe	20
	Leu	Ile	Ser	Gly	Ala	Glu	Ala	Ala	Ser	Phe	30
	Gln	Arg	Asn	Gln	Leu	Leu	Gln	Lys	Glu	Pro	40
	Asp	Leu	Arg	Leu	Glu	Asn	Val	Gln	Lys	Phe	50
	Pro	Ser	Pro	Glu	Met	Ile	Arg	Ala	Leu	Glu	60
10	Tyr	Ile	Glu	Asn	Leu	Arg	Gln	Gln	Ala	His	70
	Lys	Glu	Glu	Ser	Ser	Pro	Asp	Tyr	Asn	Pro	80
	Tyr	Gln	Gly	Val	Ser	Val	Pro	Leu	Gln	Gln	90
	Lys	Glu	Asn	Gly	Asp	Glu	Ser	His	Leu	Pro	100
	Glu	Arg	Asp	Ser	Leu	Ser	Glu	Glu	Asp	Trp	110
15	Met	Arg	Ile	Ile	Leu	Glu	Ala	Leu	Arg	Gln	120
	Ala	Glu	Asn	Glu	Pro	Gln	Ser	Ala	Pro	Lys	130
	Glu	Asn	Lys	Pro	Tyr	Ala	Leu	Asn	Ser	Glu	140
	Lys	Asn	Phe	Pro	Met	Asp	Met	Ser	Asp	Asp	150
	Tyr	Glu	Thr	Gln	Gln	Trp	Pro	Glu	Arg	Lys	160
20	Leu	Lys	His	Met	Gln	Phe	Pro	Pro	Met	Tyr	170
	Glu	Glu	Asn	Ser	Arg	Asp	Asn	Pro	Phe	Lys	180
	Arg	Thr	Asn	Glu	Ile	Val	Glu	Glu	Gln	Tyr	190
	Thr	Pro	Gln	Ser	Leu	Ala	Thr	Leu	Glu	Ser	200
	Val	Phe	Gln	Glu	Leu	Gly	Lys	Leu	Thr	Gly	210
25	Pro	Asn	Asn	Gln	Lys	Arg	Glu	Arg	Met	Asp	220
	Glu	Glu	Gln	Lys	Leu	Tyr	Thr	Asp	Asp	Glu	230
	Asp	Asp	Ile	Tyr	Lys	Ala	Asn	Asn	Ile	Ala	240
	Tyr	Glu	Asp	Val	Val	Gly	Gly	Glu	Asp	Trp	250
	Asn	Pro	Val	Glu	Glu	Lys	Ile	Glu	Ser	Gln	260
30	Thr	Gln	Glu	Glu	Val	Arg	Asp	Ser	Lys	Glu	270
	Asn	Ile	Gly	Lys	Asn	Glu	Gln	Ile	Asn	Asp	280
	Glu	Met	Lys	Arg	Ser	Gly	Gln	Leu	Gly	Ile	290
	Gln	Glu	Glu	Asp	Leu	Arg	Lys	Glu	Ser	Lys	300
	Asp	Gln	Leu	Ser	Asp	Asp	Val	Ser	Lys	Val	310
35	Ile	Ala	Tyr	Leu	Lys	Arg	Leu	Val	Asn	Ala	320
	Ala	Gly	Ser	Gly	Arg	Leu	Gln	Asn	Gly	Gln	330
	Asn	Gly	Glu	Arg	Ala	Thr	Arg	Leu	Phe	Glu	340
	Lys	Pro	Leu	Asp	Ser	Gln	Ser	Ile	Tyr	Gln	350

	Leu	Ile	Glu	Ile	Ser	Arg	Asn	Leu	Gln	Ile	360
	Pro	Pro	Glu	Asp	Leu	Ile	Glu	Met	Leu	Lys	370
	Thr	Gly	Glu	Lys	Pro	Asn	Gly	Ser	Val	Glu	380
	Pro	Glu	Arg	Glu	Leu	Asp	Leu	Pro	Val	Asp	390
5	Leu	Asp	Asp	Ile	Ser	Glu	Ala	Asp	Leu	Asp	400
	His	Pro	Asp	Leu	Phe	Gln	Asn	Arg	Met	Leu	410
	Ser	Lys	Ser	Gly	Tyr	Pro	Lys	Thr	Pro	Gly	420
	Arg	Ala	Gly	Thr	Glu	Ala	Leu	Pro	Asp	Gly	430
	Leu	Ser	Val	Glu	Asp	Ile	Leu	Asn	Leu	Leu	440
10	Gly	Met	Glu	Ser	Ala	Ala	Asn	Gln	Lys	Thr	450
	Ser	Tyr	Phe	Pro	Lys	Gln	Ile	Pro	Thr	Phe	460
	Leu	Phe	Ser	Val	Leu	Thr	Ser	Ile	Leu	Leu	470
	Thr	Leu									472